

## SEQUENCE LISTING

<110> WHITE, JOHN  
FERNANDES, ISABELLE

<120> NUCLEAR RECEPTOR TRANSCRIPTIONAL COREPRESSOR AND USES  
THEREOF

<130> BER-003US1

<140> 10/529,512

<141> 2005-03-25

<150> PCT/CA03/01477

<151> 2003-09-25

<150> 60/413,602

<151> 2002-09-26

<160> 30

<170> PatentIn Ver. 3.3

<210> 1

<211> 1828

<212> DNA

<213> Homo sapiens

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<222> (527)..(1825)

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ggagataaac accaccatca tctgagagcc gggaagggga aggcgagggt gtgtaggcgg 180
cacgaatgct ccgttgagag acgcggcttt cggcaagaac tggattcgtg gcgccacaag 240
ctcattcact gtgtagggtc cgtttccctc tgtgcggcgg ccggcgggac cataagggct 300
taactcatat atttaacccc cctccaaaaa ggtttgaaag tattcttgaa gggctgtttg 360
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attggacttt tgatgaaaac tgtttattct gttgcttgag aagagataaa gtaaagacag 480
tccctgggtc tccgaccca atattcccct agtggcccgt gagatc atg cag cga      535
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1

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atg atc caa caa ttt gct gct gaa tat acc tca aaa aat agc tct act      583
Met Ile Gln Gln Phe Ala Ala Glu Tyr Thr Ser Lys Asn Ser Ser Thr
      5              10              15
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cag gac ccc agc cag ccc aat agc aca aag aac caa agc ctg ccg aaa	631
Gln Asp Pro Ser Gln Pro Asn Ser Thr Lys Asn Gln Ser Leu Pro Lys	
20 25 30 35	
gca tct cca gtc acc acc tct ccc acg gct gca act act cag aac cct	679
Ala Ser Pro Val Thr Thr Ser Pro Thr Ala Ala Thr Thr Gln Asn Pro	
40 45 50	
gtg ctc agc aaa ctt ctc atg gct gac caa gac tca cct ctg gac ctt	727
Val Leu Ser Lys Leu Leu Met Ala Asp Gln Asp Ser Pro Leu Asp Leu	
55 60 65	
act gtc aga aag tct cag tca gaa cct agc gaa caa gac ggt gta ctt	775
Thr Val Arg Lys Ser Gln Ser Glu Pro Ser Glu Gln Asp Gly Val Leu	
70 75 80	
gat ctg tcc act aag aaa agt cca tgt gct ggc agc act tcc ctg agc	823
Asp Leu Ser Thr Lys Lys Ser Pro Cys Ala Gly Ser Thr Ser Leu Ser	
85 90 95	
cac tct cca ggc tgc tcc agt act caa ggg aac ggg cga cct ggg aga	871
His Ser Pro Gly Cys Ser Ser Thr Gln Gly Asn Gly Arg Pro Gly Arg	
100 105 110 115	
ccc agc cag tac cgc cca gac gga ctt cgg agt ggt gat ggg gta cct	919
Pro Ser Gln Tyr Arg Pro Asp Gly Leu Arg Ser Gly Asp Gly Val Pro	
120 125 130	
cca aga agc tta cag gat gga acc agg gaa ggt ttt gga cac tcc aca	967
Pro Arg Ser Leu Gln Asp Gly Thr Arg Glu Gly Phe Gly His Ser Thr	
135 140 145	
tca ctc aaa gtt cca ctg gct cga tcc ctg cag att agt gaa gaa cta	1015
Ser Leu Lys Val Pro Leu Ala Arg Ser Leu Gln Ile Ser Glu Glu Leu	
150 155 160	
ctg agc aga aac caa ttg tcc aca gct gcc agc ctt ggg cca tct gga	1063
Leu Ser Arg Asn Gln Leu Ser Thr Ala Ala Ser Leu Gly Pro Ser Gly	
165 170 175	
tta cag aat cat gga caa cac tta ata tta tcc agg gaa gcc tct tgg	1111
Leu Gln Asn His Gly Gln His Leu Ile Leu Ser Arg Glu Ala Ser Trp	
180 185 190 195	
gca aaa cca cat tac gag ttc aac ctc agc cgt atg aag ttc agg gga	1159
Ala Lys Pro His Tyr Glu Phe Asn Leu Ser Arg Met Lys Phe Arg Gly	
200 205 210	
aat ggt gca ctc agc aac atc agt gac ctt cct ttt ctt gca gaa aac	1207
Asn Gly Ala Leu Ser Asn Ile Ser Asp Leu Pro Phe Leu Ala Glu Asn	
215 220 225	
tct gcc ttt cca aaa atg gca ctt caa gca aaa caa gat gga aaa aag	1255
Ser Ala Phe Pro Lys Met Ala Leu Gln Ala Lys Gln Asp Gly Lys Lys	
230 235 240	

gac gtg agc cat tca tct cct gta gat tta aag ata cca caa gtt cga 1303  
 Asp Val Ser His Ser Ser Pro Val Asp Leu Lys Ile Pro Gln Val Arg  
 245 250 255

gga atg gat ctt tct tgg gag tct cgc act ggt gat cag tac agc tat 1351  
 Gly Met Asp Leu Ser Trp Glu Ser Arg Thr Gly Asp Gln Tyr Ser Tyr  
 260 265 270 275

agc tct ttg gta atg ggt tca caa acg gag agc gcg ctt agt aaa aaa 1399  
 Ser Ser Leu Val Met Gly Ser Gln Thr Glu Ser Ala Leu Ser Lys Lys  
 280 285 290

tta agg gct att ctt cca aaa caa agt aga aaa agc atg tta gat gct 1447  
 Leu Arg Ala Ile Leu Pro Lys Gln Ser Arg Lys Ser Met Leu Asp Ala  
 295 300 305

ggg ccc gat tct tgg ggc tca gat gct gag cag tct acc cct gga cag 1495  
 Gly Pro Asp Ser Trp Gly Ser Asp Ala Glu Gln Ser Thr Pro Gly Gln  
 310 315 320

cca tat ccc aca tcg gat caa gaa gga gac cct ggc tcc aag cag cct 1543  
 Pro Tyr Pro Thr Ser Asp Gln Glu Gly Asp Pro Gly Ser Lys Gln Pro  
 325 330 335

cgg aag aaa aga ggg cgt tac aga cag tac aac agt gag ata ctg gag 1591  
 Arg Lys Lys Arg Gly Arg Tyr Arg Gln Tyr Asn Ser Glu Ile Leu Glu  
 340 345 350 355

gaa gca atc tca gtg gtt atg agt gga aaa atg agt gtt tcc aaa gct 1639  
 Glu Ala Ile Ser Val Val Met Ser Gly Lys Met Ser Val Ser Lys Ala  
 360 365 370

cag agt att tat ggg att ccc cac agt aca ctg gag tac aaa gta aag 1687  
 Gln Ser Ile Tyr Gly Ile Pro His Ser Thr Leu Glu Tyr Lys Val Lys  
 375 380 385

gag agg ctg ggc act ttg aaa aac cct cca aag aaa aag atg aaa tta 1735  
 Glu Arg Leu Gly Thr Leu Lys Asn Pro Pro Lys Lys Lys Met Lys Leu  
 390 395 400

atg agg tcg gag ggg cca gat gtt tct gta aag att gaa tta gat ccc 1783  
 Met Arg Ser Glu Gly Pro Asp Val Ser Val Lys Ile Glu Leu Asp Pro  
 405 410 415

cag gga gag gca gca caa agt gca aat gaa tca aaa aac gag tag 1828  
 Gln Gly Glu Ala Ala Gln Ser Ala Asn Glu Ser Lys Asn Glu  
 420 425 430

<210> 2  
 <211> 433  
 <212> PRT  
 <213> Homo sapiens

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Ser Ser Thr Gln Asp Pro Ser Gln Pro Asn Ser Thr Lys Asn Gln Ser  
 20 25 30  
 Leu Pro Lys Ala Ser Pro Val Thr Thr Ser Pro Thr Ala Ala Thr Thr  
 35 40 45  
 Gln Asn Pro Val Leu Ser Lys Leu Leu Met Ala Asp Gln Asp Ser Pro  
 50 55 60  
 Leu Asp Leu Thr Val Arg Lys Ser Gln Ser Glu Pro Ser Glu Gln Asp  
 65 70 75 80  
 Gly Val Leu Asp Leu Ser Thr Lys Lys Ser Pro Cys Ala Gly Ser Thr  
 85 90 95  
 Ser Leu Ser His Ser Pro Gly Cys Ser Ser Thr Gln Gly Asn Gly Arg  
 100 105 110  
 Pro Gly Arg Pro Ser Gln Tyr Arg Pro Asp Gly Leu Arg Ser Gly Asp  
 115 120 125  
 Gly Val Pro Pro Arg Ser Leu Gln Asp Gly Thr Arg Glu Gly Phe Gly  
 130 135 140  
 His Ser Thr Ser Leu Lys Val Pro Leu Ala Arg Ser Leu Gln Ile Ser  
 145 150 155 160  
 Glu Glu Leu Leu Ser Arg Asn Gln Leu Ser Thr Ala Ala Ser Leu Gly  
 165 170 175  
 Pro Ser Gly Leu Gln Asn His Gly Gln His Leu Ile Leu Ser Arg Glu  
 180 185 190  
 Ala Ser Trp Ala Lys Pro His Tyr Glu Phe Asn Leu Ser Arg Met Lys  
 195 200 205  
 Phe Arg Gly Asn Gly Ala Leu Ser Asn Ile Ser Asp Leu Pro Phe Leu  
 210 215 220  
 Ala Glu Asn Ser Ala Phe Pro Lys Met Ala Leu Gln Ala Lys Gln Asp  
 225 230 235 240  
 Gly Lys Lys Asp Val Ser His Ser Ser Pro Val Asp Leu Lys Ile Pro  
 245 250 255  
 Gln Val Arg Gly Met Asp Leu Ser Trp Glu Ser Arg Thr Gly Asp Gln  
 260 265 270  
 Tyr Ser Tyr Ser Ser Leu Val Met Gly Ser Gln Thr Glu Ser Ala Leu  
 275 280 285  
 Ser Lys Lys Leu Arg Ala Ile Leu Pro Lys Gln Ser Arg Lys Ser Met  
 290 295 300  
 Leu Asp Ala Gly Pro Asp Ser Trp Gly Ser Asp Ala Glu Gln Ser Thr  
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<211> 60
<212> PRT
<213> Homo sapiens
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Ile Leu Glu Glu Ala Ile Ser Val Val Met Ser Gly Lys Met Ser Val
      20             25             30

Ser Lys Ala Gln Ser Ile Tyr Gly Ile Pro His Ser Thr Leu Glu Tyr
      35             40             45

Lys Val Lys Glu Arg Leu Gly Thr Leu Lys Asn Pro
  50             55             60

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<210> 4
<211> 17
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide
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<400> 4  
Gln Asp Pro Ser Gln Pro Asn Ser Thr Lys Asn Gln Ser Leu Pro Lys  
1 5 10 15

Ala

<210> 5  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 5  
 ccggaattcc ggatgaccat gaccctccac 30

<210> 6  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 6  
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<210> 7  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 7  
 ccggaattcc ggcccgggca tgagacagtc cctgggtctc 40

<210> 8  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 8  
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<210> 9  
 <211> 30  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 9  
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<210> 10  
 <211> 29  
 <212> DNA  
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<220>  
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<400> 10  
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<210> 11  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 11  
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<210> 12  
 <211> 29  
 <212> DNA  
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<220>  
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<400> 12  
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<210> 13  
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<223> Description of Artificial Sequence: Synthetic primer

<400> 13

cggaattcca gcgaatgac caacaa

26

<210> 14

<211> 33

<212> DNA

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<223> Description of Artificial Sequence: Synthetic primer

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cgcggatccg cgctactcgt tttttgattc att

33

<210> 15

<211> 7

<212> PRT

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<223> Description of Artificial Sequence: Synthetic peptide motif sequence

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Pro Leu Asp Leu Thr Val Arg

1

5

<210> 16

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide motif sequence

<400> 16

Val Leu Asp Leu Ser Thr Lys

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5

<210> 17

<211> 5

<212> PRT

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<220>

<223> Description of Artificial Sequence: Synthetic peptide



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<210> 18  
 <211> 9  
 <212> PRT  
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<220>  
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 <222> (2)  
 <223> variable amino acid

<220>  
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 <222> (4)  
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<220>  
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 <222> (6)  
 <223> variable amino acid

<220>  
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 <222> (8)  
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<400> 18  
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<210> 19  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<400> 19  
 Leu Ser Lys Leu Leu  
     1                    5

<210> 20  
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 <212> PRT  
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<220>  
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 peptide motif sequence

<400> 20  
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       1                  5

<210> 21  
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 <212> PRT  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<220>  
 <221> MOD\_RES  
 <222> (5)  
 <223> Ser or Thr

<220>  
 <221> MOD\_RES  
 <222> (6)  
 <223> variable amino acid

<220>  
 <221> MOD\_RES  
 <222> (7)  
 <223> Arg or Lys

<400> 21  
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<210> 22  
 <211> 8  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 peptide motif sequence

<220>  
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 <222> (6)..(7)  
 <223> variable amino acid

&lt;400&gt; 22

Pro Xaa Leu Asp Leu Xaa Xaa Arg  
 1 5

&lt;210&gt; 23

&lt;211&gt; 60

&lt;212&gt; PRT

<213> *Drosophila melanogaster*

&lt;400&gt; 23

Glu Gly Ile Glu Leu Ser Arg Ser Asn Pro Thr Pro Trp Ser Glu Asp  
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Ala Met Asn Glu Ala Leu Asn Ser Val Arg Leu Gly Gln Met Ser Ile  
 20 25 30

Asn Gln Ala Ala Ile His Tyr Asn Leu Pro Tyr Ser Ser Leu Tyr Gly  
 35 40 45

Arg Phe Lys Arg Gly Lys Tyr Asp Val Val Ala Asn  
 50 55 60

&lt;210&gt; 24

&lt;211&gt; 60

&lt;212&gt; PRT

<213> *Drosophila melanogaster*

&lt;400&gt; 24

Lys Gly Thr Arg Pro Lys Arg Cys Lys Tyr Arg Asn Tyr Asp Arg Asp  
 1 5 10 15

Ser Leu Val Glu Ala Val Lys Ala Val Gln Arg Gly Glu Met Ser Val  
 20 25 30

His Arg Ala Gly Ser Tyr Tyr Gly Val Pro His Ser Thr Leu Glu Tyr  
 35 40 45

Lys Val Lys Glu Arg His Leu Met Arg Pro Arg Lys  
 50 55 60

&lt;210&gt; 25

&lt;211&gt; 60

&lt;212&gt; PRT

<213> *Caenorhabditis elegans*

&lt;400&gt; 25

Lys Arg Ser Arg Pro Lys Arg Gly Gln Tyr Arg Lys Tyr Asp Lys Asn  
 1 5 10 15

Ala Leu Asp Glu Ala Val Arg Ser Val Arg Arg Gly Glu Met Thr Val  
 20 25 30

His Arg Ala Gly Ser Phe Phe Gly Val Pro His Ser Thr Leu Glu Tyr  
 35 40 45

Lys Val Lys Glu Arg Asn Leu Met Arg Lys Lys Lys  
 50 55 60

<210> 26  
 <211> 60  
 <212> PRT  
 <213> *Apis mellifera*

<400> 26  
 Lys Gly Thr Arg Pro Lys Arg Gly Lys Tyr Arg Asn Tyr Asp Arg Asp  
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 20 25 30  
 His Arg Ala Gly Ser Tyr Tyr Gly Val Pro His Ser Thr Leu Phe Tyr  
 35 40 45  
 Lys Val Lys Glu Arg His Leu Met Arg Pro Arg Lys  
 50 55 60

<210> 27  
 <211> 60  
 <212> PRT  
 <213> *Apis mellifera*

<400> 27  
 Val Pro Val Val Gly Ala Gly Gly Gly Arg Arg Ala Tyr Thr Glu Glu  
 1 5 10 15  
 Glu Leu Gln Ala Ala Leu Arg Asp Ile Gln Ser Gly Lys Leu Gly Thr  
 20 25 30  
 Arg Arg Ala Ala Val Ile Tyr Gly Ile Pro Arg Ser Thr Leu Arg Asn  
 35 40 45  
 Lys Val Tyr Lys Leu Ala Met Glu Arg Glu Arg Asp  
 50 55 60

<210> 28  
 <211> 60  
 <212> PRT  
 <213> *Drosophila melanogaster*

<400> 28  
 Ser Gly Glu Lys Gly Gly Phe Asn Gly Pro Lys Ala Trp Thr Gln Asp  
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 Asp Met Asn Ser Ala Leu Asp Ala Leu Lys Asn Gln Asn Met Ser Leu  
 20 25 30  
 Thr Lys Ala Ser Ala Ile Tyr Gly Ile Pro Ser Thr Thr Leu Trp Gln  
 35 40 45

Arg Ala His Arg Met Gly Ile Glu Thr Pro Lys Lys  
 50 55 60

<210> 29  
 <211> 60  
 <212> PRT  
 <213> Drosophila melanogaster

<400> 29  
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 Ala Leu Gln Asn Ala Leu Glu Ala Leu Arg Ser Gly Gln Ile Ser Ala  
 20 25 30  
 Asn Lys Ala Ser Lys Ala Phe Gly Ile Pro Ser Ser Thr Leu Tyr Lys  
 35 40 45  
 Ile Ala Arg Arg Glu Gly Ile Arg Leu Ala Ala Pro  
 50 55 60

<210> 30  
 <211> 60  
 <212> PRT  
 <213> Drosophila melanogaster

<400> 30  
 Arg Leu Ala Ala Pro Phe Asn Ala Ala Pro Thr Thr Trp Thr Pro Glu  
 1 5 10 15  
 Asp Leu Glu Arg Ala Leu Glu Ala Ile Arg Ala Gly Asn Thr Ser Val  
 20 25 30  
 Gln Lys Ala Ser Ala Glu Phe Gly Ile Pro Thr Gly Thr Leu Tyr Gly  
 35 40 45  
 Arg Cys Lys Arg Glu Gly Ile Glu Leu Ser Arg Ser  
 50 55 60